



Full Map

Nucleotide

Protein

Features

Annotations

History

Taxonomy

MM

Help

Search 

for

Go

Clear

Limits

Preview/Index

History

Clipboard

Details

Display

Save

Text

Add to Clipboard

Get Subsequence

1: XM\_171629. Homo sapiens simi...[gi:22062231]

Links

LOCUS LOC257238 1295 bp mRNA linear PRI 01-AUG-2002  
DEFINITION Homo sapiens similar to cortical granule serine protease 1  
precursor (LOC257238), mRNA.  
ACCESSION XM\_171629  
VERSION XM\_171629.1 GI:22062231  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1295)  
AUTHORS NCBI Annotation Project.  
TITLE Direct Submission  
JOURNAL Submitted (31-JUL-2002) National Center for Biotechnology  
Information, NIH, Bethesda, MD 20894, USA  
COMMENT GENOME ANNOTATION REFSEQ: This model reference sequence was  
predicted from NCBI contig NT\_009782 by automated computational  
analysis using gene prediction method: GenomeScan, supported by EST  
evidence.  
Also see:  
Documentation of NCBI's Annotation Process

FEATURES Location/Qualifiers  
source 1..1295  
organism="Homo sapiens"  
db\_xref="taxon:9606"  
chromosome="11"  
gene 1..1295  
gene="LOC257238"  
db\_xref="InterimID:257238"  
CDS 168..1295  
gene="LOC257238"  
codon\_start=1  
product="similar to cortical granule serine protease 1  
precursor"  
protein\_id="XP\_171629.1"

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note="Region: smart00020, Tryp\_SPc, Trypsin-like serine protease; Many of these are synthesised as inactive precursor zymogens that are cleaved during limited proteolysis to generate their active forms. A few, however, are active as single chain molecules, and others are inactive due to substitutions of the catalytic triad residues"

misc\_feature 171..434  
gene="LOC257238"

misc\_feature 819..1199  
note="Region: pfam00089, trypsin, Trypsin"  
gene="LOC257238"

misc\_feature 900..1187  
note="Region: pfam02395, IGA1, Immunoglobulin A1 protease. This family consists of immunoglobulin A1 protease proteins. The immunoglobulin A1 protease cleaves immunoglobulin IgA and is found in pathogenic bacteria such as *Neisseria gonorrhoeae*. Not all of the members of this family are IgA proteases (one member from *E. coli* cleaves human coagulation factor V, another one is a hemoglobin protease)"  
gene="LOC257238"

misc\_feature 903..1187  
note="Region: smart00020, Tryp\_SPc, Trypsin-like serine protease; Many of these are synthesised as inactive precursor zymogens that are cleaved during limited proteolysis to generate their active forms. A few, however, are active as single chain molecules, and others are inactive due to substitutions of the catalytic triad residues"

variation 681  
gene="LOC257238"  
allele="C"  
allele="T"  
db\_xref="dbSNP:3742071"

BASE COUNT 352 a 265 c 314 g 364 t  
ORIGIN

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61 aagcacaagc tgggcgatgg ccttgggggg tgagcctgca gattaaatat gcccggttc
121 ttttcatgt atgttgggga acctagtgga gagagagcga tctttaaagc tggacagctg
181 tgaatgggaa taaatataaa cctggagcgt atctcctaac caagaagata aaaattaaag
241 caatcattat tcacccaaac ttcatttttg aatcttatgt aaatgatatt gcacttttcc
301 acttaaaaaa agcagtggag tataatgact atattcagcc tatttgccca ccttttgatg
361 ttttccaaat cctggacgga aacacaaaag gttttataag tggctgggga agaacaaaag
421 aagaaggtat agcaggtctt gtgactgtgg tgtcctgtgg tctttacaag ctaaagtaca
481 gaadagatga gaaaatgtra attcatttta ttcacatgaq agttctgtgc caaggatttg
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1261 ctttatgttt tgtcatttta cttagcaacaa cataa

//

Revised: July 5, 2002.

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12/4/2002

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Query: 215  GNATNIIQQDAEVHYISREMCNSERSYGGIIP:NTSFCAGDEDGAFDTCRGDSGGPLMCOYLP 274
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Sbjct: 900  GNATNIIQQDAEVHYISREMCNSERSYGGIIP:NTSFCAGDEDGAFDTCRGDSGGPLMCOYLP 1079

Query: 275  EYERFFVMGITSYGHGCGREGFPGVYIGPSFYQKWLTEHFFHASTQGILTINILFGQILI 334
           EYERFFVMGITSYGHGCGREGFPGVYIGPSFYQKWLTEHFFHASTQGILTINILFGQILI
Sbjct: 1080 EYERFFVMGITSYGHGCGREGFPGVYIGPSFYQKWLTEHFFHASTQGILTINILFGQILI 1259

Query: 335  ALCFVILLATT 345
           ALCFVILLATT
Sbjct: 1260 ALCFVILLATT 1292

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>XM\_171629 ACCESSION:XM\_171629 NID: gi 22062231 ref XM\_171629.1 Homo  
sapiens similar to cortical granule serine protease 1  
precursor (LOC257238), mRNA  
Length = 1295

Identities = 141/153 (92%), Positives = 141/153 (92%)  
Frame = +3

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          CGTAPLKDVLQGSRIIGSTEAGAGAWPWVSLQIKYGRVLVHVCGGTLVFE
Sbjct: 3   CGTAPLKDVLQGSRIIGSTEAGAGAWPWVSLQIKYGRVLVHVCGGTLVFE----- 155
          ↓
Query: 122 TKDS DPLMWTAVIGTNNIHGRYPHTKKIKIKAI IHPNFILESYVNDIALFHLKKAVFYN 181
          SDPLMWTAVIGTNNIHGRYPHTKKIKIKAI IHPNFILESYVNDIALFHLKKAVFYN
Sbjct: 156 ---SDPLMWTAVIGTNNIHGRYPHTKKIKIKAI IHPNFILESYVNDIALFHLKKAVFYN 326

Query: 182 DYIQPICLPFDVVFQILDGNTYCFISGWGETKEE 214
          DYIQPICLPFDVVFQILDGNTYCFISGWGETKEE
Sbjct: 327 DYIQPICLPFDVVFQILDGNTYCFISGWGETKEE 427
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Identities = 131/131 (100%), Positives = 131/131 (100%)  
Frame = +3

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Query: 215  GNATNILQDAEVHYISREMCNUSERSYGGIIPNTSFCAGDEDGAFDTCRGDSSGGPLMCYLP 274
          GNATNILQDAEVHYISREMCNUSERSYGGIIPNTSFCAGDEDGAFDTCRGDSSGGPLMCYLP
Sbjct: 900  GNATNILQDAEVHYISREMCNUSERSYGGIIPNTSFCAGDEDGAFDTCRGDSSGGPLMCYLP 1079

Query: 275  EYKRFFVMGITSYGHGCGRFGFPGVYIGPSFYQKWLTEHFFHASTQGILTINILRGQILI 334
          EYKRFFVMGITSYGHGCGRFGFPGVYIGPSFYQKWLTEHFFHASTQGILTINILRGQILI
Sbjct: 1080 EYKRFFVMGITSYGHGCGRFGFPGVYIGPSFYQKWLTEHFFHASTQGILTINILRGQILI 1259

Query: 335  ALCFVILLATT 345
          ALCFVILLATT
Sbjct: 1260 ALCFVILLATT 1292
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